

## SEQUENCE LISTING

<110> White, David  
Zhou, Jianghong  
Tartaglia, Louis A.

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<140> US 09/195,896

<141> 1998-11-19

<150> US 60/108,379

<151> 1998-10-29

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 Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys  
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 Tyr Tyr Ile Pro Glu Val Phe Tyr Thr Gly Val Tyr Pro Pro Tyr Ala  
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 Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly  
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 Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Lys Asn Ile Cys Ser  
          355                         360                         365  
 Tyr Ile Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile  
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&lt;211&gt; 365

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&lt;213&gt; Mus musculus

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Pro	Asp	Arg	Phe	Lys	Asp	Phe	Leu	Leu	Tyr	Leu	Arg	Cys	Arg	Asn	Tyr
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 Thr Gly Ser Gly Lys Ser Phe Ile Asn Thr Leu Arg Gly Ile Gly  
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 Asn Glu Glu Glu Gly Ala Ala Lys Thr Gly Val Val Glu Val Thr Met  
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 Glu Lys Met Lys Phe Tyr Glu Tyr Asp Phe Phe Ile Ile Ile Ser Ala  
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 Thr Arg Phe Lys Lys Asn Asp Ile Asp Ile Ala Lys Ala Ile Ser Met  
 145 150 155 160  
 Met Lys Lys Glu Phe Tyr Phe Val Arg Thr Lys Val Asp Ser Asp Ile  
 165 170 175  
 Thr Asn Glu Ala Asp Gly Lys Pro Gln Thr Phe Asp Lys Glu Lys Val  
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Leu Gln Asp Ile Arg Leu Asn Cys Val Asn Thr Phe Arg Glu Asn Gly  
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 Ile Ala Glu Pro Pro Ile Phe Leu Leu Ser Asn Lys Asn Val Cys His  
 210 215 220  
 Tyr Asp Phe Pro Val Leu Met Asp Lys Leu Ile Ser Asp Leu Pro Ile  
 225 230 235 240  
 Tyr Arg Arg His Asn Phe Met Val Ser Leu Pro Asn Ile Thr Asp Ser  
 245 250 255  
 Val Ile Glu Lys Lys Arg Gln Phe Leu Lys Gln Arg Ile Trp Leu Glu  
 260 265 270  
 Gly Phe Ala Ala Asp Leu Val Asn Ile Ile Pro Ser Leu Thr Phe Leu  
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 Leu Asp Ser Asp Leu Glu Thr Leu Lys Lys Ser Met Lys Phe Tyr Arg  
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 Thr Val Phe Gly Val Asp Glu Thr Ser Leu Gln Arg Leu Ala Arg Asp  
 305 310 315 320  
 Trp Glu Ile Glu Val Asp Gln Val Glu Ala Met Ile Lys Ser Pro Ala  
 325 330 335  
 Val Phe Lys Pro Thr Asp Glu Glu Thr Ile Gln Glu Arg Leu Ser Arg  
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 Tyr Ile Gln Glu Phe Cys Leu Ala Asn Gly Tyr Leu Leu Pro Lys Asn  
 355 360 365  
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 Met Val Glu Gln Glu Ser Gln Ile Phe His Asp Ile Ile Val Glu Asp  
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 Arg Trp Val Ala Thr Phe Cys Ser Lys Ala Lys Tyr Val Met Lys Thr  
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 Asp Ser Asp Ile Phe Val Asn Met Asp Asn Leu Ile Tyr Lys Leu Leu  
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 His Thr Arg Leu Leu His Leu Glu Asp Val Tyr Val Gly Leu Cys Leu  
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 Arg Lys Leu Gly Ile His Pro Phe Gln Asn Ser Gly Phe Asn His Trp  
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 Lys Met Ala Tyr Ser Leu Cys Arg Tyr Arg Arg Val Ile Thr Val His  
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 Arg Gln Asp Phe Leu Asp Thr Tyr Asn Asn Leu Thr Leu Lys Thr Ile  
 145 150 155 160  
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 180 185 190  
 Tyr Leu Leu Asn Leu Asn His Ser Glu Lys Phe Phe Thr Gly Tyr Pro  
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 210 215 220  
 Ser Tyr Gln Glu Tyr Pro Phe Lys Val Phe Pro Pro Tyr Cys Ser Gly  
 225 230 235 240  
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 245 250 255  
 Met Ser His Val Lys Pro Ile Lys Phe Glu Asp Val Tyr Val Gly Ile  
 260 265 270  
 Cys Leu Asn Leu Leu Lys Val Asp Ile His Ile Pro Glu Asp Thr Asn  
 275 280 285  
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 Gly Ser Gly Ser Ala Ser Ser Gly Leu Asp Lys Phe Ala Tyr Leu Arg  
 50 55 60  
 Val Pro Ser Phe Thr Ala Glu Val Pro Val Asp Gln Pro Ala Arg Leu  
 65 70 75 80  
 Thr Met Leu Ile Lys Ser Ala Val Gly Asn Ser Arg Arg Arg Glu Ala  
 85 90 95  
 Ile Arg Arg Thr Trp Gly Tyr Glu Gly Arg Phe Ser Asp Val His Leu  
 100 105 110  
 Arg Arg Val Phe Leu Leu Gly Thr Ala Glu Asp Ser Glu Lys Asp Val  
 115 120 125  
 Ala Trp Glu Ser Arg Glu His Gly Asp Ile Leu Gln Ala Asp Phe Thr  
 130 135 140  
 Asp Ala Tyr Phe Asn Asn Thr Leu Lys Thr Met Leu Gly Met Arg Trp  
 145 150 155 160  
 Ala Ser Glu Gln Phe Asn Arg Ser Glu Phe Tyr Leu Phe Val Asp Asp  
 165 170 175  
 Asp Tyr Tyr Val Ser Ala Lys Asn Val Leu Lys Phe Leu Gly Arg Gly  
 180 185 190  
 Arg Gln Ser His Gln Pro Glu Leu Leu Phe Ala Gly His Val Phe Gln  
 195 200 205

Thr	Ser	Pro	Leu	Arg	His	Lys	Phe	Ser	Lys	Trp	Tyr	Val	Ser	Leu	Glu
	210					215					220				
Glu	Tyr	Pro	Phe	Asp	Arg	Trp	Pro	Pro	Tyr	Val	Thr	Ala	Gly	Ala	Phe
225					230					235					240
Ile	Leu	Ser	Gln	Lys	Ala	Leu	Arg	Gln	Leu	Tyr	Ala	Ala	Ser	Val	His
				245						250				255	
Leu	Pro	Leu	Phe	Arg	Phe	Asp	Asp	Val	Tyr	Leu	Gly	Ile	Val	Ala	Leu
			260					265					270		
Lys	Ala	Gly	Ile	Ser	Leu	Gln	His	Cys	Asp	Asp	Phe	Arg	Phe	His	Arg
		275					280					285			
Pro	Ala	Tyr	Lys	Gly	Pro	Asp	Ser	Tyr	Ser	Ser	Val	Ile	Ala	Ser	His
	290					295					300				
Glu	Phe	Gly	Asp	Pro	Glu	Glu	Met	Thr	Arg	Val	Trp	Asn	Glu	Cys	Arg
305					310					315					320
Ser	Ala	Asn	Tyr	Ala											
				325											

<210> 11  
 <211> 422  
 <212> PRT  
 <213> Homo sapien

<400> 11															
Met	Leu	Gln	Trp	Arg	Arg	Arg	His	Cys	Cys	Phe	Ala	Lys	Met	Thr	Trp
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Asn	Ala	Lys	Arg	Ser	Leu	Phe	Arg	Thr	His	Leu	Ile	Gly	Val	Leu	Ser
			20					25					30		
Leu	Val	Phe	Leu	Phe	Ala	Met	Phe	Leu	Phe	Phe	Asn	His	His	Asp	Trp
		35				40					45				
Leu	Pro	Gly	Arg	Ala	Gly	Phe	Lys	Glu	Asn	Pro	Val	Thr	Tyr	Thr	Phe
	50					55					60				
Arg	Gly	Phe	Arg	Ser	Thr	Lys	Ser	Glu	Thr	Asn	His	Ser	Ser	Leu	Arg
65					70					75					80
Asn	Ile	Trp	Lys	Glu	Thr	Val	Pro	Gln	Thr	Leu	Arg	Pro	Gln	Thr	Ala
			85					90					95		
Thr	Asn	Ser	Asn	Asn	Thr	Asp	Leu	Ser	Pro	Gln	Gly	Val	Thr	Gly	Leu
			100					105					110		
Glu	Asn	Thr	Leu	Ser	Ala	Asn	Gly	Ser	Ile	Tyr	Asn	Glu	Lys	Gly	Thr
		115					120				125				
Gly	His	Pro	Asn	Ser	Tyr	His	Phe	Lys	Tyr	Ile	Ile	Asn	Glu	Pro	Glu
	130					135					140				
Lys	Cys	Gln	Glu	Lys	Ser	Pro	Phe	Leu	Ile	Leu	Leu	Ile	Ala	Ala	Glu
145					150					155					160
Pro	Gly	Gln	Ile	Glu	Ala	Arg	Arg	Ala	Ile	Arg	Gln	Thr	Trp	Gly	Asn
			165					170					175		
Glu	Ser	Leu	Ala	Pro	Gly	Ile	Gln	Ile	Thr	Arg	Ile	Phe	Leu	Leu	Gly
			180					185					190		
Leu	Ser	Ile	Lys	Leu	Asn	Gly	Tyr	Leu	Gln	Arg	Ala	Ile	Leu	Glu	Glu
		195					200					205			
Ser	Arg	Gln	Tyr	His	Asp	Ile	Ile	Gln	Gln	Glu	Tyr	Leu	Asp	Thr	Tyr
	210					215					220				
Tyr	Asn	Leu	Thr	Ile	Lys	Thr	Leu	Met	Gly	Met	Asn	Trp	Val	Ala	Thr
225					230					235					240
Tyr	Cys	Pro	His	Ile	Pro	Tyr	Val	Met	Lys	Thr	Asp	Ser	Asp	Met	Phe
				245					250					255	
Val	Asn	Thr	Glu	Tyr	Leu	Ile	Asn	Lys	Leu	Leu	Lys	Pro	Asp	Leu	Pro
			260					265					270		
Pro	Arg	His	Asn	Tyr	Phe	Thr	Gly	Tyr	Leu	Met	Arg	Gly	Tyr	Ala	Pro
		275					280					285			
Asn	Arg	Asn	Lys	Asp	Ser	Lys	Trp	Tyr	Met	Pro	Pro	Asp	Leu	Tyr	Pro
	290					295					300				



Ser Glu Arg Tyr Pro Val Phe Cys Ser Gly Thr Gly Tyr Val Phe Ser  
 305 310 315 320  
 Gly Asp Leu Ala Glu Lys Ile Phe Lys Val Ser Leu Gly Ile Arg Arg  
 325 330 335  
 Leu His Leu Glu Asp Val Tyr Val Gly Ile Cys Leu Ala Lys Leu Arg  
 340 345 350  
 Ile Asp Pro Val Pro Pro Pro Asn Glu Phe Val Phe Asn His Trp Arg  
 355 360 365  
 Val Ser Tyr Ser Ser Cys Lys Tyr Ser His Leu Ile Thr Ser His Gln  
 370 375 380  
 Phe Gln Pro Ser Glu Leu Ile Lys Tyr Trp Asn His Leu Gln Gln Asn  
 385 390 395 400  
 Lys His Asn Ala Cys Ala Asn Ala Ala Lys Glu Lys Ala Gly Arg Tyr  
 405 410 415  
 Arg His Arg Lys Leu His  
 420

<210> 12  
 <211> 229  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> VARIANT  
 <222> (1)...(229)  
 <223> Xaa = Any Amino Acid

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 Val Xaa Leu Xaa Xaa Phe Xaa Phe Leu Xaa His Trp Phe Pro  
 20 25 30  
 Ile Trp Tyr Leu Ser Ile Pro Leu Arg Pro Gln Thr Gly Ser Xaa Ser  
 35 40 45  
 Xaa Ser Xaa Xaa Leu Ser His Leu Tyr Asn Thr Val Xaa Arg Xaa Asn  
 50 55 60  
 Xaa Xaa Phe Asn Asn Xaa Xaa Thr Arg Pro Ile Asn Ser Xaa Xaa Phe  
 65 70 75 80  
 Glu Phe Leu Ile Asp Glu Pro Xaa Lys Cys Xaa Lys Lys Pro Phe Leu  
 85 90 95  
 Val Leu Leu Ile Lys Ser Xaa Pro Gly Xaa Phe Xaa Ala Arg Gln Ala  
 100 105 110  
 Ile Arg Glu Thr Trp Gly Xaa Glu Xaa Asn Phe Xaa Gly Ile Xaa Val  
 115 120 125  
 Xaa Arg Val Phe Leu Leu Gly Lys Xaa Ala Glu Xaa Xaa Asp Pro Xaa  
 130 135 140  
 Leu Xaa Xaa Met Val Glu Xaa Glu Ser Arg Xaa His Gly Asp Ile Ile  
 145 150 155 160  
 Gln Gln Asp Phe Leu Asp Thr Tyr Phe Asn Leu Thr Leu Lys Thr Leu  
 165 170 175  
 Met Gly Met Arg Trp Val Ala Thr Phe Cys Pro Xaa Ala Glu Tyr Val  
 180 185 190  
 Met Lys Thr Asp Ser Asp Val Phe Val Asn Thr Xaa Asn Leu Leu Asn  
 195 200 205  
 Lys Leu Leu Lys Pro Ser Leu Ser His Arg Xaa Xaa Leu Phe Thr Gly  
 210 215 220  
 Tyr Val Ile Xaa Gly  
 225

<210> 13  
 <211> 1707  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (246)...(1436)

&lt;221&gt; misc feature

&lt;222&gt; (1)...(1707)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 13

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acgcgtccgc gcagcggcag cggcagcagc ggcaacaagt gccggaggct agcagagcca      60
agccggagca gtccctgccg ccgacaccgc cgggcccgcc gtccggggcg ccgcgcatgg      120
agcgtgagct gcggcggtcg ccgggctgag ccgcgcggag cggccgggac gtggatgtgg      180
ccgcgatctc ccgcccttgc ccccgccccg ccgagctgga gctgctcccg gacaagatat      240
gagaa atg agt gtt gga cgt cga aga ata aag ttg ttg ggt atc ctg atg      290
Met Ser Val Gly Arg Arg Arg Ile Lys Leu Leu Gly Ile Leu Met
      1           5           10           15

atg gca aat gtc ttc att tat ttt att atg gaa gtc tcc aaa agc agt      338
Met Ala Asn Val Phe Ile Tyr Phe Ile Met Glu Val Ser Lys Ser Ser
      20           25           30

agc caa gaa aaa aat gga aaa ggg gaa gta ata ata ccc aaa gag aag      386
Ser Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys
      35           40           45

ttc tgg aag ata tct acc cct ccc gag gca tac tgg aac cga gag caa      434
Phe Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln
      50           55           60

gag aag ctg aac cgg cag tac aac ccc atc ctg agc atg ctg acc aac      482
Glu Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn
      65           70           75

cag acg ggg gag gcg ggc agg ctc tcc aat ata agc cat ctg aac tac      530
Gln Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr
      80           85           90

tgc gaa cct gac ctg agg gtc acg tcg gtg gtt acg ggt ttt aac aac      578
Cys Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn
      100          105          110

ttg ccg gac aga ttt aaa gac ttt ctg ctg tat ttg aga tgc cgc aat      626
Leu Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn
      115          120          125

tat tca ctg ctt ata gat cag ccg gat aag tgt gca aag aaa cct ttc      674
Tyr Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe
      130          135          140

ttg ttg ctg gcg att aag tcc ctc act cca cat ttt gcc aga agg caa      722
Leu Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Arg Gln
      145          150          155

gca atc cgg gaa tcc tgg ggc caa gaa agc aac gca ggg aac caa acg      770
Ala Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr
      160          165          170

gtg gtg cga gtc ttc ctg ctg ggc cag aca ccc cca gag gac aac cac      818
Val Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His
      180          185          190

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ccc gac ctt tca gat atg ctg aaa ttt gag agt gag aag cac caa gac Pro Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp 195 200 205	866
att ctt atg tgg aac tac aga gac act ttc ttc aac ttg tct ctg aag Ile Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys 210 215 220	914
gaa gtg ctg ttt ctc agg tgg gta agt act tcc tgc cca gac act gag Glu Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu 225 230 235	962
ttt gtt ttc aag ggc gat gac gat gtt ttt gtg aac acc cat cac atc Phe Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile 240 245 250 255	1010
ctg aat tac ttg aat agt tta tcc aag acc aaa gcc aaa gat ctc ttc Leu Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe 260 265 270	1058
ata ggt gat gtg atc cac aat gct gga cct cat cgg gat aag aag ctg Ile Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu 275 280 285	1106
aag tac tac atc cca gaa gtt gtt tac tct ggc ctc tac cca ccc tat Lys Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr 290 295 300	1154
gca ggg gga ggg ggg ttc ctc tac tcc ggc cac ctg gcc ctg agg ctg Ala Gly Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu 305 310 315	1202
tac cat atc act gac cag gtc cat ctc tac ccc att gat gac gtt tat Tyr His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr 320 325 330 335	1250
act gga atg tgc ctt cag aaa ctc ggc ctc gtt cca gag aaa cac aaa Thr Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys 340 345 350	1298
ggc ttc agg aca ttt gat atc gag gag aaa aac aaa aat aac atc tgc Gly Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys 355 360 365	1346
tcc tat gta gat ctg atg tta gta cat agt aga aaa cct caa gag atg Ser Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met 370 375 380	1394
att gat att tgg tct cag ttg cag agt gct cat tta aaa tgc Ile Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys 385 390 395	1436
taaaatagat acaaactcaa tttkgsatwg raaggggtwt tttgratwgg ycccatgttg gggtctcaca ttagagtaat ttctatttna ancatgaaat tgcctttatg agtgataccc atttanggcc tctaancctt catttgnact cacgtgaaga agggaaagcg ggagaaggta attnttttat ggtgaatggc aggatattgg tctgacttac cgntagggga ntttaaaact ggnccttttt gaatctgttt ggaatggccct t	1496 1556 1616 1676 1707

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

Met	Ser	Val	Gly	Arg	Arg	Arg	Ile	Lys	Leu	Leu	Gly	Ile	Leu	Met	Met
1				5					10					15	
Ala	Asn	Val	Phe	Ile	Tyr	Phe	Ile	Met	Glu	Val	Ser	Lys	Ser	Ser	Ser
			20					25					30		
Gln	Glu	Lys	Asn	Gly	Lys	Gly	Glu	Val	Ile	Ile	Pro	Lys	Glu	Lys	Phe
		35					40					45			
Trp	Lys	Ile	Ser	Thr	Pro	Pro	Glu	Ala	Tyr	Trp	Asn	Arg	Glu	Gln	Glu
	50					55					60				
Lys	Leu	Asn	Arg	Gln	Tyr	Asn	Pro	Ile	Leu	Ser	Met	Leu	Thr	Asn	Gln
	65				70					75					80
Thr	Gly	Glu	Ala	Gly	Arg	Leu	Ser	Asn	Ile	Ser	His	Leu	Asn	Tyr	Cys
				85					90					95	
Glu	Pro	Asp	Leu	Arg	Val	Thr	Ser	Val	Val	Thr	Gly	Phe	Asn	Asn	Leu
			100					105					110		
Pro	Asp	Arg	Phe	Lys	Asp	Phe	Leu	Leu	Tyr	Leu	Arg	Cys	Arg	Asn	Tyr
		115					120					125			
Ser	Leu	Leu	Ile	Asp	Gln	Pro	Asp	Lys	Cys	Ala	Lys	Lys	Pro	Phe	Leu
	130					135					140				
Leu	Leu	Ala	Ile	Lys	Ser	Leu	Thr	Pro	His	Phe	Ala	Arg	Arg	Gln	Ala
	145					150				155					160
Ile	Arg	Glu	Ser	Trp	Gly	Gln	Glu	Ser	Asn	Ala	Gly	Asn	Gln	Thr	Val
				165					170					175	
Val	Arg	Val	Phe	Leu	Leu	Gly	Gln	Thr	Pro	Pro	Glu	Asp	Asn	His	Pro
			180					185					190		
Asp	Leu	Ser	Asp	Met	Leu	Lys	Phe	Glu	Ser	Glu	Lys	His	Gln	Asp	Ile
		195					200					205			
Leu	Met	Trp	Asn	Tyr	Arg	Asp	Thr	Phe	Phe	Asn	Leu	Ser	Leu	Lys	Glu
	210					215					220				
Val	Leu	Phe	Leu	Arg	Trp	Val	Ser	Thr	Ser	Cys	Pro	Asp	Thr	Glu	Phe
	225				230					235					240
Val	Phe	Lys	Gly	Asp	Asp	Val	Phe	Val	Asn	Thr	His	His	Ile	Leu	
				245				250					255		
Asn	Tyr	Leu	Asn	Ser	Leu	Ser	Lys	Thr	Lys	Ala	Lys	Asp	Leu	Phe	Ile
			260					265					270		
Gly	Asp	Val	Ile	His	Asn	Ala	Gly	Pro	His	Arg	Asp	Lys	Lys	Leu	Lys
		275					280					285			
Tyr	Tyr	Ile	Pro	Glu	Val	Val	Tyr	Ser	Gly	Leu	Tyr	Pro	Pro	Tyr	Ala
	290					295					300				
Gly	Gly	Gly	Gly	Phe	Leu	Tyr	Ser	Gly	His	Leu	Ala	Leu	Arg	Leu	Tyr
	305				310					315					320
His	Ile	Thr	Asp	Gln	Val	His	Leu	Tyr	Pro	Ile	Asp	Asp	Val	Tyr	Thr
				325					330					335	
Gly	Met	Cys	Leu	Gln	Lys	Leu	Gly	Leu	Val	Pro	Glu	Lys	His	Lys	Gly
			340					345					350		
Phe	Arg	Thr	Phe	Asp	Ile	Glu	Glu	Lys	Asn	Lys	Asn	Asn	Ile	Cys	Ser
			355				360					365			
Tyr	Val	Asp	Leu	Met	Leu	Val	His	Ser	Arg	Lys	Pro	Gln	Glu	Met	Ile
	370					375					380				
Asp	Ile	Trp	Ser	Gln	Leu	Gln	Ser	Ala	His	Leu	Lys	Cys			
	385				390					395					

&lt;210&gt; 15

&lt;211&gt; 365

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

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 Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln Glu  
 20 25 30  
 Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn Gln  
 35 40 45  
 Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr Cys  
 50 55 60  
 Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn Leu  
 65 70 75 80  
 Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr  
 85 90 95  
 Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe Leu  
 100 105 110  
 Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Arg Gln Ala  
 115 120 125  
 Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr Val  
 130 135 140  
 Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His Pro  
 145 150 155 160  
 Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp Ile  
 165 170 175  
 Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu  
 180 185 190  
 Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu Phe  
 195 200 205  
 Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile Leu  
 210 215 220  
 Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe Ile  
 225 230 235 240  
 Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys  
 245 250 255  
 Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr Ala  
 260 265 270  
 Gly Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu Tyr  
 275 280 285  
 His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr  
 290 295 300  
 Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly  
 305 310 315 320  
 Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys Ser  
 325 330 335  
 Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile  
 340 345 350  
 Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys  
 355 360 365

&lt;210&gt; 16

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; Artificial sequence

&lt;222&gt; (1)...(20)

&lt;223&gt; Synthetically generated primer

&lt;400&gt; 16

cttcgacgcc ccacactcat

<210> 17  
<211> 20  
<212> DNA  
<213> Homo sapiens

<220>  
<221> Artificial sequence  
<222> (1)...(20)  
<223> Synthetically generated primer

<400> 17  
atgagtgtgg ggcgtcgaag

20

Sub  
C1  
cont